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Sampling stored-product insect pests: a comparison of four statistical sampling models for probability of pest detection

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Abstract

BACKGROUND: Developing sampling strategies to target biological pests such as insects in stored grain is inherently difficult owing to species biology and behavioural characteristics. The design of robust sampling programmes should be based on an underlying statistical distribution that is sufficiently flexible to capture variations in the spatial distribution of the target species.

RESULTS: Comparisons are made of the accuracy of four probability-of-detection sampling models – the negative binomial model,[1] the Poisson model,[1] the double logarithmic model[2] and the compound model[3] – for detection of insects over a broad range of insect densities. Although the double log and negative binomial models performed well under specific conditions, it is shown that, of the four models examined, the compound model performed the best over a broad range of insect spatial distributions and densities. In particular, this model predicted well the number of samples required when insect density was high and clumped within experimental storages.

CONCLUSIONS: This paper reinforces the need for effective sampling programs designed to detect insects over a broad range of spatial distributions. The compound model is robust over a broad range of insect densities and leads to substantial improvement in detection probabilities within highly variable systems such as grain storage.

Keywords: grains; heterogeneity; Poisson; negative binomial; double logarithmic model; compound model

1 INTRODUCTION

Developing robust sampling programmes for biological systems that capture the innate variability in the system in question is inherently complex.[4] Biological organisms can be difficult to target for numerous reasons. For example, organisms may vary their distributions over space and time, influencing detection rates.[3,5] This suggests that the design of the sampling programme and the underlying statistical distribution used need to be sufficiently flexible to capture variations in the spatial and temporal distribution of the target species. Furthermore, the area that is to be sampled may not always be conducive to sampling owing to site accessibility constraints, among other factors. Therefore, to increase sampling efficiency, the statistical framework and sampling programme should be capable of being used under a broad range of conditions.

An area that has seen significant research with regards to sampling ecology has been stored-grain insects.[2,3,5–7] The presence of insects in stored grain is problematic, as they lead to restrictions in trade on account of biosecurity concerns, commodity losses and spoilage.[8–10] Therefore, sampling in stored grains has typically been undertaken to meet two distinct objectives: (a) to estimate the mean density of insects for integrated pest management (IPM); (b) for pest detection. Pest detection is necessary for pest management decisions within the grain industries, as many exporting and importing countries have a zero tolerance threshold when sampling grain shipments.[8] Additionally, in recent years, an increased emphasis on exotic pest invasion has heightened biosecurity efforts. Detection methods also provide useful tools when attempting to detect particular species or types of insect within stored grain, and thus can be used for resistance monitoring programmes.

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However, targeting insects within storages is complex because, although grain stored in various storage structures may appear to be homogeneous, insects that infest grain bulks can display varied spatial distributions, and will often be clustered.[11,12] The distribution of insects within a storage will also vary from species to species, between storage types, as a result of treatment and fumigation measures and in relation to external and internal climatic conditions.[11–14] It is therefore essential that specific sampling methods are utilised to determine the correct number of samples to be taken from a predetermined area while sampling within a heterogeneous system.

Typically in ecology, detection approaches developed where species are clustered are based on Poisson or the negative binomial probability functions.[1] The negative binomial approach considers species clustering behaviour via the incorporation of a dispersion parameter. While the Poisson does not explicitly or implicitly consider species clustering behaviour, the simple function based on mean density has been demonstrated to provide a good approximation to the negative binomial in certain instances.[1] Hagstrum *et al*.[2] found that the relationship between the probability of insect detection and the average insect density in grain is described by a double logarithmic model. This model is based on a two-step process. The first step considers 'the logarithmic increase in sample units occupied by more than one insect with an increase in mean density', and the second step considers the 'logarithmic increase in the number of insects occupying the infested sample units'.[15] Subramanyam *et al*.[7] illustrated that the model accurately predicted mean densities based on the relative proportion of sample units containing insects, explaining 84–90% of variation in mean densities. This model has therefore historically formed the basis of a number of grain sampling programmes.[2,5,7,10,13]

More recently, Elmouttie *et al*.[3] adapted an alternative methodology based on an explicit translation of the clustering behaviour of pests into a statistical function for use in stored grain. Rather than considering sample-to-sample variation, this method considers that stored grain can be separated into two distinct components. The spatially heterogeneous distribution of insects within a storage and the density of the pests have been shown to have an important influence on pest detection.[3] These quantities can be estimated in a straightforward way, and this model considers them directly. Using this model, Elmouttie *et al*.[3] demonstrated a method for determining sampling effort by directly considering the density of individuals and the level of heterogeneity within a sampled area. While the methods of Hagstrum *et al*.[2] and Elmouttie *et al*.[3] have been shown to be useful, it is as yet unknown under which conditions each of these models should be used and whether there are conditions where models either over- or underpredict the number of samples required.

The aim of this paper is therefore to compare the four described statistical sampling models to determine which models estimate the correct number of samples for a given probability of detection under a range of insect distribution. Using historical data from an extensive sampling programme of farm storages by Flinn *et al*.,[16] comparisons are made of the Poisson, the negative binomial, the double logarithmic model and the compound model developed by Elmouttie *et al*.[3] Given that insect pests occur at a range of densities in a range of environmental conditions, these comparisons have been made to determine which models are robust enough to use under a wide variety of environmental conditions.

2 MATERIALS AND METHODS

2.1 Data

The data used in this study were collected over a 7 month period commencing in July 2002 and were reported by Flinn *et al*.[16] In brief, four independent vertical bins, located in Kansas, United States, with a diameter of approximately 4.75 m and containing on average 30 t of wheat, were sampled monthly. Each bin was artificially infested monthly with 400 individuals of three insect species, *Rhyzopertha dominica*, *Cryptolestes ferrugineus* and *Tribolium castaneum*, between July and October 2002. Two independent bins each had been allocated to two distinct treatments, namely control (bins were not aerated) and aeration (bins were aerated on a regular basis). Sampling was conducted using a pneumatic grain sampler (Probe-A-Vac®; Cargill, Minneapolis, MN). An intensive monthly sampling programme was conducted, with twenty-one 3 kg samples drawn from each bin on each sampling occasion, seven samples from each of three height strata (0–0.8 m, 0.8–1.6 m, 1.6–2.4 m). In each stratum, three samples were drawn 0.3 m from the bin centre, and four samples 0.6 m from the bin wall. All samples were processed using an Insectomat® motorized inclined sieve (Samplex Ltd, Willow Park, UK) to separate insects from grain. The number of live adult insects of each species was counted in each sample immediately after extraction. For each species in each bin, a total of 21 samples × 7 occasions = 154 counts of live adult insects were available for analysis.

2.2 Model parameter estimation

The four sampling models used were: (i) the compound model (CM) proposed by Elmouttie *et al*.;[3] (ii) a negative binomial model (NBM) proposed by Green and Young;[1] (iii) a Poisson model (PM) proposed for sampling by Green and Young;[1] (iv) the double logarithmic model (DLM) proposed by Hagstrum *et al*.[2] The models represent a range of commonly utilised models to determine the number of samples in biological systems, agricultural systems and in the field of acceptance sampling.[1–3,17] For each individual model, the corresponding parameters were estimated separately (see below) for each species, bin and sampling occasion from the associated 21 insect counts. In addition, parameter estimates were obtained for the total insect numbers (ignoring species) for each bin and sampling occasion, resulting in a total of (3 species + all-species total) × 4 bins × 7 occasions = 112 sets of parameter estimates per model.

As described by Subramanyam and Hagstrum,[15] parameters *A*, *B* and *C* for the DLM were estimated for each of the four bins using the non-linear least-squares (*nls*) regression function in R.[18] The rate of infestation (λ) for the CM is representative of the mean density (insects kg^{-1} wheat samples) of insects within the infested portion of the grain bulk. Hence, for a particular sampling period, λ was calculated by dividing the sum of live insects in positive samples (samples containing insects) by the number of positive samples. For the negative binomial, PM and DLM, the sample mean ($\overline{x}$) represents the mean density throughout all samples, that is, both positive samples containing live insects and negative samples without live insects. Hence, $\overline{x}$ for these models was calculated by calculating the sum of all insects within all samples divided by the total number of samples for a sampling event, i.e. 21. For example, if 42 insects were detected in the 21 samples drawn, $\overline{x}$ would be 2 (42/21). The dispersion parameter of the negative binomial was calculated using the method described by

Southwood and Henderson[19] and illustrated in equation (2b). This methodology ensured that each model had individually generated parameter estimates from corresponding datasets (experimental bins).

The resulting parameter estimates were then used according to the following equations to calculate the number of samples (n) required to achieve a desired power of $1 - \beta$, where $\beta = 0.05$ represents the probability of a type 2 error, i.e. failing to detect an insect in n samples, and hence acceptance is governed by a zero tolerance approach. This was again done separately for each species, silo and sampling occasion.

2.2.1 *Compound model*

For the CM, the number of samples is given by

$$n_{\text{cm}} = \frac{log\beta}{\log\left(1 - p + p\,\mathrm{e}^{-w\lambda}\right)} \tag{1}$$

where p is the proportion of infested samples within a bin, w represents the weight of the sample drawn (kg) and λ represents the mean density of insects in the infested portion of the samples.

2.2.2 *Negative binomial model*

For the NBM, the number of samples is given by

$$n_{\text{nbm}} = -\frac{1}{k}\frac{log\beta}{\log\left(1 + \frac{\overline{x}}{k}\right)} \tag{2a}$$

where $\overline{x}$ is the mean density of insects throughout the lot, and k represents a dispersion parameter that can be estimated using the method presented by Southwood and Henderson,[19] that is

$$k = \left(\frac{\overline{x}^2}{s^2 + \overline{x}}\right) \tag{2b}$$

where s represents the standard deviation of insect numbers between samples.

2.2.3 *Poisson model*

For the PM, the number of samples is given by

$$n_{\text{pm}} = -\frac{1}{\overline{x}} log\beta \tag{3}$$

2.2.4 *Double logarithmic model*

For the DLM, the number of samples is given by

$$n_{\text{dlm}} = \frac{log\beta}{\log\left(1 - q\right)} \tag{4a}$$

where q is the probability of a sample having no insects, which is given by

$$q = 1 - (A\,\mathrm{e})^{(-B\overline{x})} + (1 - A)\;\mathrm{e}^{(-C\overline{x})} \tag{4b}$$

where parameters A, B and C describe the relationship between the proportion of sample units that are infested and the mean density of insects.

2.3 Model comparisons

A Monte Carlo simulation study consisting of 10 000 iterations was undertaken to determine which of the four models performed best across each individual dataset (four experimental bins). At each iteration, one individual bin was randomly selected and the number of samples (n) for each model was calculated as described above. The number of samples was then used to select randomly from the companion experimental bin with the same treatment – this was done for each model. For example, consider the trial with a Poisson model. Parameter estimates for the Poisson model were obtained using the data from control bin 1, and the number of samples was calculated from this. This number of samples was subsequently used to sample randomly from control bin 2 (with replacement from the 21 available counts) over the same sampling occasion. This methodology provided independence between the parameter estimates and the data that were sampled, such that a bin used to estimate the number of samples was not sampled in an individual simulation experiment. A detection was recorded when at least one of the n samples drawn contained at least one insect. The number of detections from the 10 000 iterations was recorded and the percentage detection rate was determined. Simulations were not conducted for any model when zero insects were detected for a particular time period in either companion bin.

Chi-square (χ^2) analyses were used to determine any statistically significant differences in the percentage detection rates between different models. Root mean square errors (RMSEs) were also calculated to measure the differences between the expected probability of detection ($\beta = 0.95$) and the values observed from the simulation results for each model. This provided a measure of accuracy for each model to the expected 0.95 probability of detection. RMSE is given by

$$\text{RMSE} = \sqrt{\sum \frac{\left[\left(\beta - \widehat{\beta}\right)^2\right]}{nc}} \tag{5}$$

where β is the expected value (0.95) and $\widehat{\beta}$ is the observed value, and nc represents the number of combinations (expected versus observed) compared.

3 RESULTS

Mean insect densities varied between treatments, sampling periods and insect species (Table 1). In general, insect population densities increased throughout the experimental period, reaching their highest in the months of October and November (Table 1). A notable decline in insect densities was recorded in aerated bins from November to January, and this also corresponded to a reduction in sample units with insects (Table 1).

Simulations were not conducted for the July sampling period in control and aeration bins, as bins 1, 2 and 4 had no insects detected for this period. Similarly, simulations were not conducted for aeration bins in December, as zero insects were detected in one bin for this period (Table 1).

The number of samples n varied across models, with those needed for the PM being consistently lower than the three other models examined (Table 2). Across the four models examined, mean percentage insect detection with n grain samples did not differ significantly when data from control bins were examined (Table 3). This pattern was consistent when species data

Table 1. Mean ± 1 SE insect densities across all treatments within four independent grain bins. The number in parentheses represents the total number of subsamples (3 kg) containing insects of the 21 samples drawn in each sampling event

		Aeration		Control	
Species	Time	Bin 1	Bin2	Bin 3	Bin4
R. dominica	July	0.00 (0)	0.00 (0)	0.047 ± 0.21 (1)	0.00 (0)
C. ferrugineus	July	0.00 (0)	0.00 (0)	0.00 (0)	0.00 (0)
T. castaneum	July	0.00 (0)	0.00 (0)	0.00 (0)	0.047 ± 0.21 (1)
R. dominica	August	0.33 ± 0.57 (6)	0.28 ± 0.46 (6)	0.66 ± 0.85 (10)	0.23 ± 0.43 (5)
C. ferrugineus	August	0.14 ± 0.35 (3)	0.14 ± 0.35 (3)	0.23 ± 0.53 (4)	0.047 ± 0.21 (1)
T. castaneum	August	0.47 ± 1.03 (5)	0.66 ± 1.01 (8)	1.76 ± 3.49 (11)	0.23 ± 0.53 (4)
R. dominica	September	2.81 ± 4.33 (8)	10.19 ± 19.77 (16)	28 ± 14.18 (21)	25.47 ± 17.39 (21)
C. ferrugineus	September	0.95 ± 1.32 (10)	0.76 ± 1.37 (7)	3.85 ± 3.59 (16)	0.85 ± 0.85 (13)
T. castaneum	September	2.38 ± 3.16 (14)	2.09 ± 3.85 (13)	3.33 ± 3.29 (18)	7.66 ± 7.53 (20)
R. dominica	October	24.47 ± 19.03 (21)	45.19 ± 40.58 (20)	169 ± 88.26 (21)	176.33 ± 127.38 (21)
C. ferrugineus	October	5.09 ± 5.82 (14)	4.42 ± 5.97 (16)	37.66 ± 25.12 (21)	9.61 ± 8.07 (18)
T. castaneum	October	1.66 ± 1.90 (15)	2.61 ± 4.34 (15)	12.00 ± 14.18 (17)	12.57 ± 12.78 (19)
R. dominica	November	15.76 ± 15.63 (17)	58.8 ± 107.42 (21)	96.14 ± 68.53 (21)	138.28 ± 100.69 (21)
C. ferrugineus	November	0.42 ± 1.16 (4)	0.66 ± 1.27 (5)	89.09 ± 81.49 (21)	44.47 ± 28.41 (21)
T. castaneum	November	1.00 ± 1.78 (10)	2.61 ± 5.28 (13)	9.38 ± 16.59 (20)	12.85 ± 23.81 (19)
R. dominica	December	0.00 (0)	24.38 ± 72.79 (5)	43.52 ± 33.20 (21)	109.61 ± 68.23 (21)
C. ferrugineus	December	0.00 (0)	0.33 ± 1.06 (2)	96.04 ± 115.12 (20)	76.90 ± 101.48 (21)
T. castaneum	December	0.00 (0)	1.00 ± 1.34 (10)	6.00 ± 10.55 (14)	13.80 ± 28.19 (15)
R. dominica	January	1.47 ± 4.47 (4)	16.66 ± 49.62 (6)	45.90 ± 46.37 (21)	127.80 ± 125.67 (21)
C. ferrugineus	January	0.095 ± 0.300 (2)	0.00 (0)	388.95 ± 861.21 (19)	65.47 ± 68.95 (19)
T. castaneum	January	0.095 ± 0.30 (2)	0.47 ± 0.98 (5)	30.23 ± 83.82 (19)	5.09 ± 3.65 (18)

simulations were compared independently or in combination in control bins, with the exception of the PM for *T. castaneum* in control bins 1 and 2 (Table 3). In contrast, however, the PM differed from all other models across all species when examining aeration bin data (Table 3). This was a result of the lower insect densities within aeration bins (Table 1). No significant difference in mean percentage detections were recorded between the DLM, NB and CM models for either individual species comparisons or combined simulation comparisons (Table 3).

RMSE estimates show that, although the four models did not differ significantly, the CM typically had a lower RMSE than the other models tested (Table 4). Across all treatment and species combinations, the CM generally had the lowest RMSE estimates. This corresponded to a higher number of samples typically being estimated by the compound model (Table 2). The NB model, however, had the lowest RMSE on five occasions, although differences in RMSE between the NB and CM were very small over these five periods (Tables 3 and 4).

To this point, simulation results for each simulation have been grouped across all time periods. However, insect densities varied significantly throughout the study in control and aeration bins, as did the distribution of insects in the grain bins (inferred from the number of containing insects) (Table 1). Although mean percentage success was constantly lower for the PM, prediction was most accurate during the August sampling period and did not differ significantly from other models during this period (Table 3). During all sampling periods the CM performed well and was the most or second most accurate model tested (Tables 3 and 5). The NBM and DLM performed well in four of the five sampling periods and were not statistically different from the CM model over these four periods. In the January sampling period, however, where insect density was relatively high although restricted to a limited portion of the grain lot, prediction fell well below the 0.95 threshold for the NBM and DLM (Table 3). Results for the CM differed significantly from the DLM and NBM for the January period and were closest to the 0.95 detection threshold. Further, RMSE estimates illustrate that the CM was the most accurate model over three of the five time periods examined and always ranked in the top two models.

4 DISCUSSION AND CONCLUSIONS

Over the broad range of insect densities examined in this study, the CM proposed by Elmouttie *et al.*[3] consistently achieved a probability of detection closer to 0.95 than any other models tested. Other models performed slightly better in some circumstances (see Table 5, September and October); however, when this occurred, the difference in RMSE between the best performing model and the CM was small. The CM was the most robust model of all tested, across a range of spatial distributions and insect densities. This illustrates the flexibility of the CM, as it is a model that is suitable for detecting insects over a range of insect spatial distributions. There are a number of difficulties when developing sampling programmes for biological and agricultural systems. Firstly, the environment that is sampled is often heterogeneous, leading to irregular usage of space by the target species. This is further complicated by the fact that the level of heterogeneity or the level of irregularity is often difficult to perceive or quantify. Secondly, target species may have specific behaviours (mobility, preference for moisture, dockage, etc.) that may give rise to varied distribution and densities of the target species within the area being sampled. It is therefore important to develop sampling protocols based on an understanding and statistical design that can encompass a broad range of possible spatial distributions.

Table 2. The number of samples *n* required for 95% probability of insect detection as generated from each model[a] for each sampling species combination

		Aeration bin 1				Aeration bin 2				Control bin 3				Control bin 4			
Time	Species	CM	NBM	PM	DLM	CM	NBM	PM	DLM	CM	NBM	PM	DLM	CM	NBM	PM	DLM
Aug	*R.dominica*	14	7	9	11	15	9	10	14	7	5	4	5	18	11	13	14
Aug	*C. ferrugineus*	32	20	21	24	32	20	21	26	21	14	13	14	98	41	63	67
Aug	*T. castaneum*	13	10	6	9	8	6	4	7	4	5	2	3	21	14	13	14
Sep	*R.dominica*	3	3	1	4	2	3	1	3	1	1	1	1	1	1	1	1
Sep	*C. ferrugineus*	6	4	3	6	8	6	4	6	2	2	1	2	5	3	3	4
Sep	*T. castaneum*	3	3	1	4	3	4	1	3	2	2	1	4	1	1	1	1
Oct	*R.dominica*	1	1	1	1	1	1	1	2	1	1	1	1	1	1	1	1
Oct	*C. ferrugineus*	3	2	1	3	2	2	1	3	1	1	1	1	2	1	1	1
Oct	*T. castaneum*	3	3	2	4	3	4	1	3	2	1	1	1	1	1	1	1
Nov	*R.dominica*	2	1	1	2	1	2	1	1	1	1	1	1	1	1	1	1
Nov	*C. ferrugineus*	16	13	7	9	12	7	4	7	1	1	1	1	1	1	1	1
Nov	*T. castaneum*	6	6	3	5	3	5	1	3	1	3	1	2	1	3	1	1
Dec	*R.dominica*	—	—	—	—	11	5	1	2	1	1	1	1	1	1	1	1
Dec	*C. ferrugineus*	—	—	—	—	16	18	9	12	1	1	1	1	1	1	1	1
Dec	*T. castaneum*	—	—	—	—	6	4	3	5	3	3	1	2	2	3	1	1
Jan	*R.dominica*	14	10	2	5	9	5	1	2	1	1	1	1	1	1	1	1
Jan	*C. ferrugineus*	48	30	31	35	—	—	—	—	1	2	1	1	1	1	1	1
Jan	*T. castaneum*	48	30	31	35	13	9	6	9	1	4	1	1	2	1	1	2

[a] CM – compound model; NBM – negative binomial model; PM – Poisson model; DL – double logarithmic model.

Here, four statistical sampling models were compared, two proposed for grain sampling[2,3] and two used commonly for broader ecological purposes.[1] Of the four models examined, the Poisson model consistently underpredicted the number of samples required to detect insects at a 0.95 probability of detection level. This is not surprising, as it is the most restrictive model and does not contain a mechanism to capture or describe clustering or heterogeneity. The PM consistently underpredicted the number of samples required, particularly within aeration bins, where insect density was found to be more patchily distributed albeit often locally abundant (Tables 1 and 2). This is problematic for insect sampling, as it is not uncommon for insects to be heterogeneously distributed in grain masses,[11] although at a relatively high density, violating the assumption of the Poisson. Therefore, density-based approaches such as the Poisson will tend to underestimate the number of samples required for detection when sampling for a target that is not at very low densities.

In contrast, the NBM, DLM and CM performed well, with prediction typically reaching the desired 0.95 probability of detection threshold. The NBM and DLM, however, were not as robust as the CM in extreme situations where many samples contained no insects but positive samples contained a high density of insects. In such instances, the DLM and NBM underpredicted the number of samples required to detect insects. In Table 3 it is shown that the mean detection success declined dramatically for the NBM and DLM in the January sampling period. This corresponded to data representing very high population densities within a small number of samples, resulting in data that were highly skewed (Table 1). Although mechanistically different, the NBM and DLM were most similar of all models tested. This was observed in both mean percentage simulation success and RMSE estimates. Hagstrum *et al.*[2] previously noted this, showing that, of a range of models tested, the DLM and NBM characterised a range of data most closely.

As found in the present study, insect distribution and density can vary significantly within storages (Table 1). Of all models tested, the CM performed well consistently, predicting an adequate number of samples to detect at the desired 0.95 probability of detection over a broad range of data. The model was found not to be overly influenced by population mean or variance attributes. For the CM, a higher predicted value for the number of samples *n* (when compared with the other models) resulted in a probability of detection closer to the desired 0.95 level. Not surprisingly, when multiple models reached the equivalent probability of detection, the number of samples predicted was also similar (Table 2). This illustrates that using the CM does not result in added effort (a greater number of samples) without a corresponding increase in probability of detection. The results from RMSE analysis (Tables 4 and 5) show that the CM is the most effective and accurate model to use for the detection of insects within grain storages.

An added benefit of the CM is the direct biological relevance of the parameters. Although models such as the DLM and NBM can be used to estimate the number of samples, the parameters required are often difficult to estimate. This may be, in part, why Poisson and binomial-based approaches have gained such popularity in the literature.[17,19] Although these approaches often do not best describe the system or provide the most robust estimates for the number of samples required, model parameters are easily estimated. Similarly to the NBM and DLM, the CM proposed by Elmouttie *et al.*[3] requires estimation of multiple parameters: p – the proportion of infestation; λ – the mean density within the infested portion of the site. However, unlike the DLM and NBM, parameters in the CM can be simply estimated from data and do not require statistical or computational expertise. The approach used here, for example, could be used in a real storage system containing grain stored in multiple bins or bunkers. Grain producers or bulk handlers/elevator managers could intensively sample a single storage to develop parameter estimates and,

Table 3. Mean (±1 SE) percentage insect detections for all simulation combinations and χ^2 significance at $P = 0.05$. Numbers in italic bold indicate models that are significantly different from the model closest to 95% probability of detection[a]

Month	Treatment	Bin	Species	CM	NBM	PM	DLM	χ^2 [b]
Combined	Control	3	Combined	91.00 ± 0.027	91.44 ± 0.032	84.28 ± 0.043	88.67 ± 0.037	n
Combined	Control	3	*R. dominica*	96.67 ± 0.024	94.67 ± 0.044	93.50 ± 0.055	94.83 ± 0.043	n
Combined	Control	3	*C. ferrugineus*	88.33 ± 0.055	86.50 ± 0.080	81.50 ± 0.092	85.67 ± 0.078	n
Combined	Control	3	*T. castaneum*	88.00 ± 0.065	93.17 ± 0.056	***77.83 ± 0.092***	85.50 ± 0.081	y
Combined	Control	4	Combined	96.22 ± 0.012	95.72 ± 0.014	94.44 ± 0.020	94.83 ± 0.020	n
Combined	Control	4	*R. dominica*	100.00 ± 0.00	99.83 ± 0.002	97.17 ± 0.016	99.83 ± 0.001	n
Combined	Control	4	*C. ferrugineus*	97.33 ± 0.016	97.00 ± 0.016	***86.17 ± 0.049***	97.33 ± 0.016	y
Combined	Control	4	*T. castaneum*	91.33 ± 0.032	90.33 ± 0.032	***86.17 ± 0.049***	87.33 ± 0.054	n
Combined	Aeration	1	Combined	91.02 ± 0.021	88.50 ± 0.036	***69.14 ± 0.061***	85.57 ± 0.050	y
Combined	Aeration	1	*R. dominica*	91.06 ± 0.036	90.40 ± 0.064	***72.40 ± 0.147***	***81.80 ± 0.125***	y
Combined	Aeration	1	*C. ferrugineus*	94.50 ± 0.026	89.00 ± 0.048	***77.75 ± 0.095***	91.75 ± 0.049	y
Combined	Aeration	1	*T. castaneum*	88.20 ± 0.043	86.20 ± 0.077	***59.00 ± 0.054***	84.40 ± 0.068	y
Combined	Aeration	2	Combined	97.50 ± 0.007	95.14 ± 0.014	***84.79 ± 0.043***	95.93 ± 0.015	y
Combined	Aeration	2	*R. dominica*	98.20 ± 0.008	95.80 ± 0.017	***82.40 ± 0.095***	94.20 ± 0.037	y
Combined	Aeration	2	*C. ferrugineus*	96.25 ± 0.021	91.25 ± 0.038	***84.00 ± 0.067***	94.25 ± 0.025	y
Combined	Aeration	2	*T. castaneum*	97.80 ± 0.011	97.60 ± 0.009	***87.80 ± 0.068***	99.00 ± 0.003	y
August	Aeration	1 & 2	Combined	97.33 ± 0.016	92.17 ± 0.028	90.33 ± 0.048	96.00 ± 0.022	n
September	Aeration	1 & 2	Combined	94.33 ± 0.017	93.83 ± 0.028	***71.67 ± 0.044***	96.00 ± 0.013	y
October	Aeration	1 & 2	Combined	96.00 ± 0.015	95.50 ± 0.018	***83.00 ± 0.057***	97.50 ± 0.009	y
November	Aeration	1 & 2	Combined	92.75 ± 0.030	93.83 ± 0.036	***79.00 ± 0.090***	88.50 ± 0.039	y
December	Aeration	1 & 2	Combined	0.00	0.00	0.00	0.00	n/a
January	Aeration	1 & 2	Combined	89.25 ± 0.064	***78.50 ± 0.103***	***52.75 ± 0.167***	***68.25 ± 0.142***	y

[a] CM – compound model; NBM – negative binomial model; PM – Poisson model; DL – double logarithmic model.
[b] Significant at $P = 0.05$; y = yes; n = no.

Table 4. Root mean square errors ($\beta = 0.95$) for all sampling models[a] for each species and combined species data in both aeration and control bins. Numbers in bold represent the most accurate models (i.e. lowest RMSE)

		Model[b]			
Species	Treatment	CM	NBM	PM	DLM
R .dominica	Aeration bin 1	**0.0823***	0.1362	0.3698	0.2824
C. ferrugineus	Aeration bin 1	**0.0458***	0.1017	0.2395	0.0912
T. castaneum	Aeration bin 1	**0.1101***	0.1777	0.3758	0.1733
R. dominica	Aeration bin 2	0.0363	**0.0346***	0.2296	0.0743
C. ferrugineus	Aeration bin 2	**0.0384***	0.0753	0.1602	0.0433
T. castaneum	Aeration bin 2	0.0352	**0.0326***	0.1543	0.0405
R. dominica	Control bin 3	**0.0577***	0.0987	0.1252	0.0950
C. ferrugineus	Control bin 3	**0.1409***	0.1985	0.2457	0.1986
T. castaneum	Control bin 3	0.1626	**0.1273***	0.2679	0.2064
R. dominica	Control bin 4	0.0500	**0.0485***	0.0500	**0.0485***
C. ferrugineus	Control bin 4	0.0440	**0.0408***	0.0426	0.0440
T. castaneum	Control bin 4	**0.0802***	0.0856	0.1407	0.1431
Combined	Control bin 3	**0.1286***	0.1476	0.2220	0.1742
Combined	Control bin 4	**0.0602***	0.0615	0.0897	0.0909
Combined	Aeration bin 1	**0.0857***	0.1444	0.3401	0.2039
Combined	Aeration bin 2	**0.0365***	0.0493	0.1861	0.556

[a] CM – compound model; NBM – negative binomial model; PM – Poisson model; DL – double logarithmic model.
[b] An asterisk (*) indicates the model with the lowest RMSE.

using those estimates, determine the number of samples needed to sample adjoining storages adequately. Alternatively, parameter estimates for CM parameters p and λ could be developed from prior information or expert opinion, as they have a direct biological relevance.[20] This would be significantly more difficult when developing estimates for parameter k in the negative binomial model or for parameters A, B and C in the double logarithmic model, as they are based on an interaction between multiple factors.

The present study has demonstrated the importance of using a statistical sampling model that is robust and based on a broad range of data. Using data over a broad temporal scale, it was

Table 5. Root mean square errors ($\beta = 0.95$) for all sampling models[a] using combined species data for each sampling period in aeration bins. Numbers in bold represent the most accurate models (i.e. lowest RMSE)

		Model[b]			
Species	Treatment	CM	NBM	PM	DLM
August	Aeration	**0.0440***	0.0704	0.1187	0.0507
September	Aeration	0.0383	0.0644	0.2540	**0.0306***
October	Aeration	0.0361	0.0398	0.1760	**0.0324***
November	Aeration	**0.0716***	0.0838	0.2753	0.1095
December	Aeration	—	—	—	—
January	Aeration	**0.1250***	0.2352	0.5124	0.3629

[a] CM – compound model; NBM – negative binomial model; PM – Poisson model; DL – double logarithmic model.
[b] An asterisk (*) indicates the model with the lowest RMSE.

possible to show the importance of considering length of storage and grain temperature, as insect density will increase with time, and distributions vary in relation to external factors. In large grain-producing countries such as Australia, the United States and Canada, these factors will be influenced by local climate and environment. It is therefore important to acquire robust sampling data across a geographic and seasonal continuum so that better parameter estimates can be developed to improve sampling models. These data, coupled with a robust statistical model such as the CM, will ensure that sampling programmes are adequate and utilise the correct number of samples for detection at the desired level.

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REFERENCES

1 Green RH and Young RC, Sampling to detect rare species. *Ecol Applic* **3**:351–356 (1993).
2 Hagstrum DW, Milliken GA and Waddell MS, Insect distribution in bulk-stored wheat in relation to detection or estimation of abundance. *Environ Entomol* **14**:655–661 (1985).
3 Elmouttie D, Kiermeier A and Hamilton G, Improving detection probabilities in stored grain. *Pest Manag Sci* **66**:1280–1286 (2010).
4 Pillar VD, Sampling sufficiency in ecological surveys. *Abstr Bot* **22**:37–48 (1998).
5 Lippert GE and Hagstrum DW, Detection or estimation of insect population in bulk-stored wheat with probe traps. *J Econ Entomol* **80**:601–604 (1987).
6 Hunter AJ and Griffith HJ, Bayesian approach to estimation of insect population size. *Technometrics* **20**:231–234 (1978).
7 Subramanyam BH, Hagstrum DW and Schenk TC, Sampling adult beetles (Coleoptera) associated with stored grain – comparing detection and mean trap catch efficiency of two types of probe traps. *Environ Entomol* **22**:33–42 (1993).
8 Jefferies GM, *Review of grain sampling inspection methodology*. Department of Agriculture, Fisheries and Forestry, Australia (2000).
9 Rees D, *Insects of Stored Products*. CSIRO Publishing, Melbourne, Vic, Australia (2004).
10 Hagstrum DW and Subramanyam B, *Fundamentals in Stored-Product Entomology*. AACC International Press, St Paul, MN (2006).
11 Athanassiou CG, Kavallieratos NG, Palyvos NE and Buchelos CT, Three dimensional distribution and sampling indices of insects and mites in horizontally-stored wheat. *Appl Entomol Zool* **38**:413–426 (2003).
12 Nansen C, Flinn P, Hagstum D, Toews MD and Meikle WG, Interspecific associations among stored-grain beetles. *J Stored Prod Res* **45**:254–260 (2009).
13 Hagstrum DW, Seasonal variation of stored wheat environment and insect population. *Environ Entomol* **16**:77–83 (1987).
14 Cuperus GW, Fargo WS, Flinn PW and Hagstrem DW, Variables affecting capture of stored-grain insects in probe traps. *J Kans Entomol Soc* **63**:486–489 (1990).
15 Subramanyam B and Hagstrum DW, *Integrated Management of Insects in Stored Products*. Marcel Dekker, New York, NY (1996).
16 Flinn PW, Subramanyam BH and Arthur FH, Comparison of aeration and spinosad for suppressing insects in stored wheat. *J Econ Entomol* **97**:1465–1473 (2004).
17 Stephens KS, *The Handbook of Applied Acceptance Sampling: Plans, Principles and Procedures*. American Society for Quality, Milwaukee, WI (2001).
18 *R: A Language and Environment for Statistical Computing*. [Online]. R Development Core Team. R Foundation for Statistical Computing, Vienna, Austria (2010). Available: http://www.r-project.org/ Accessed [3 June 2012].
19 Southwood TRE and Henderson PA, *Ecological Methods*. Blackwell Science, Carlton, Vic, Australia (2000).
20 Martin TG, Kuhnert PM, Mengersen K and Possingham HP, The power of expert opinion in ecological models using Bayesian methods: impact of grazing on birds. *Ecol Applic* **15**:266–280 (2005).

